

110677

Schreiber, David

From: Ramirez, Delia
Sent: Monday, December 15, 2003 6:47 PM
To: Schreiber, David
Subject: case 09/866379

Hi,

I would like to request the following alignments:

1. seq id 5, 6, 7 against seq id 9 (nucleic acids)
2. seq id 8 against seq id 10 (proteins)
3. seq id 8 against seq id 7
4. seq id 10 against seq id 9

Thank you,

De' M. Ramirez, Ph.D.
Patent Examiner
Recombinant Enzymes-Art Unit 1652
USPTO
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Arlington, VA 22202
(703) 306-0288
delia.ramirez@uspto.gov


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Qy 841 CGCAGCGAGGTGTCCGCGCGCGCCACCGTATATAGATTGATCAGCAGCG 900
Db 1028 CGCAGCGAGGTGTCCGCGCGCGCCACCGTATATAGATTGATCAGCAGCG 1087
Qy 901 TTGACGCCCATCCACCAAAAACGCGGTATATACCACTTACAGTGTG 960
Db 1088 TTGACGCCCATCCACCAAAAACGCGGTATATACCACTTACAGTGTG 1147
Qy 961 TTATATCGCGACACATATATATCGCAATCTCGCGCGCGTACAGTGTG 1020
Db 1148 TTATATCGCGACACATATATATCGCAATCTCGCGCGCGTACAGTGTG 1207
Qy 1021 AGCTTCCTCGGTACGAGTAAACACCGCGCGTACAGTGTG 1080
Db 1208 AGCTTCCTCGGTACGAGTAAACACCGCGCGTACAGTGTG 1267
Qy 1081 CTTGCGGTACGAGTAAACACCGCGCGTACAGTGTG 1140
Db 1268 CTTGCGGTACGAGTAAACACCGCGCGTACAGTGTG 1327
Qy 1141 CAGTGTGTGATTAACACCGCGCGTACAGTGTG 1200
Db 1328 CAGTGTGTGATTAACACCGCGCGTACAGTGTG 1387
Qy 1201 CTTGCGGTACGAGTAAACACCGCGCGTACAGTGTG 1260
Db 1388 CTTGCGGTACGAGTAAACACCGCGCGTACAGTGTG 1447
Qy 1261 AGCTTCCTCGGTACGAGTAAACACCGCGCGTACAGTGTG 1300
Db 1448 AGCTTCCTCGGTACGAGTAAACACCGCGCGTACAGTGTG 1487

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RESULT 2

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; Sequence 5: Application US/09866379C
; GENERAL INFORMATION:
; APPLICANT: Short, Kevin A.
; APPLICANT: Gray, Kevin A.
; APPLICANT: Barton, Nelson Robert
; APPLICANT: O'Neil, Thomas J.
; APPLICANT: O'Neil, Thomas J.
; APPLICANT: Mathur, Eric J.
; TITLE OF INVENTION: RECOMBINANT BACTERIAL PHYTASES AND USES
; TITLE OF INVENTION: THIS REPORT
; CURRENT APPLICATION NUMBER: US/09/866,379C
; PRIOR FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 09/580,515
; PRIOR APPLICATION NUMBER: US 09/318,528
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: US 09/291,931
; PRIOR FILING DATE: 1999-04-04
; PRIOR APPLICATION NUMBER: US 09/259,214
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: US 08/910,798
; PRIOR FILING DATE: 1997-08-13
; PRIOR APPLICATION NUMBER: US 08/910,798
; SOFTWARE: PASC-SEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1901
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 403
; ORGANIZATION: n = A,T,C or G
; US-09-866-379C-5

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Query Match 96.9%; Score 1267; DB 1; Length 1901;
Best Local Similarity 98.4%; Fred. No. 0;

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Matches 1279; Conservative 0; Mismatches 21; Indels 0; Gaps 0;
Qy 1 ATGAAAGCGCTATATCCCAATTTTATCTCTCTGCGTATACCGCGCATCTGCA 60
Db 188 ATGAAAGCGCTATATCCCAATTTTATCTCTCTGCGTATACCGCGCATCTGCA 247
Qy 61 TTCTCTCAGATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 120
Db 248 TTCTCTCAGATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 307
Qy 121 GTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 180
Db 308 GTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 367
Qy 181 ACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 240
Db 368 ACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 427
Qy 241 GCGATCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300
Db 428 GCGATCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 487
Qy 301 GCGATCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 360
Db 488 GCGATCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 547
Qy 361 GCGATCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 420
Db 548 GCGATCTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 607
Qy 421 TCGAGTCCCGATCGGTATTTATCTCTTAAACCTGCGTTCGCACTGATACGCG 480
Db 608 TCGAGTCCCGATCGGTATTTATCTCTTAAACCTGCGTTCGCACTGATACGCG 667
Qy 481 AACCTGCTGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 540
Db 668 AACCTGCTGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 727
Qy 541 TATCAGCGCGGTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
Db 728 TATCAGCGCGGTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 787
Qy 601 CTTAACTCTGAGAACGAGCAGCAAGCTGTTATTAACGCGCGCGCGCGCGCGCGCG 660
Db 788 CTTAACTCTGAGAACGAGCAGCAAGCTGTTATTAACGCGCGCGCGCGCGCGCGCG 847
Qy 661 ATGCTGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
Db 848 ATGCTGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 907
Qy 721 GAGATTTCTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
Db 908 GAGATTTCTCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 967
Qy 781 GATTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 840
Db 968 GATTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1027
Qy 841 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 900
Db 1028 CCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1087
Qy 901 TTAATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 960
Db 1088 TTAATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1147
Qy 961 TTTATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1020
Db 1148 TTTATCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1207
Qy 1021 AGCTTCCTCGGTACGAGTAAACACCGCGCGTACAGTGTG 1080
Db 1208 AGCTTCCTCGGTACGAGTAAACACCGCGCGTACAGTGTG 1267

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Cy 1261 ATCTGATGAGCAGCGNTACCGGTCGAGTTTGAGT 1300
Db 1448 ATCTGATGAGCAGCGNTACCGGTCGAGTTTGAGT 1487

Search completed: December 18, 2003, 08:46:30
Job time : 5 secs


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QY 381 GlnMetArgAspLysThrProLeuSerIleuAsnThrProProGlyGluValIysLeuThr 400
DB 1328 CAAATGCGTGTATTAACCCGCTGTCTATTAATACCCGCTCTCCGAGGAGTGAACAGCC 1397
QY 401 LeuAlaGlyCysGluGluArgAsnAlaGlnGlyMetCysSerIleuAlaGlyPheThrGln 420
DB 1388 CTGCGAGGTGTGAAACCCAAATGCCAGGCGGTGTGCTGTCCGACGTTTATCCCA 1447
QY 421 IleValAsnGluAlaArgIleProAlaCysSerIleu 432
DB 1448 ATGTGATGAGCGCCATACCGGCTCCAGTTG 1483

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Search completed: December 18, 2003, 08:56:07
 Job time : 3 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 18, 2003, 08:49:27 Search time 0.001 Seconds
(66.624 Million cell updates/sec)

Title: us-09-866-379c-8
Parent score: 32.6
Sequence: 1 MKALLPFLSLILPLPQSA.....CSLAGFTQIYNERTIPACSL 432

Scoring table: BLOSUM62 Gapop 10.0, Gapext 0.5
Searched: 1 seqs, 432 residues
Total number of hits satisfying chosen parameters: 1
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1 summaries

Database : us-09-866-379c-10+
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query No.	Score	Match	Length	DB ID	Description
1	2182	97.2	432	1	us-09-866-379c-10	

ALIGNMENTS

RESULT 1	us-09-866-379c-10					
Query Match	97.2%	Score 2182	DB 1	Length 432		
Percent Similarity	98.1%	Positives 32.0				
Matches 424	Conservative	0	Mismatches 8	Indels 0	Gaps 0	
QY	1	MKALLPFLSLILPLPQSA.....CSLAGFTQIYNERTIPACSL 432				
DB	1	MKALLPFLSLILPLPQSA.....CSLAGFTQIYNERTIPACSL 432				
QY	61	TKWVLEWTFVRSGLIYNGTQKVADELAVKQVSSQVLLADVDSTRTES 120				
DB	61	TKWVLEWTFVRSGLIYNGTQKVADELAVKQVSSQVLLADVDSTRTES 120				
QY	121	AFAGELAPOLITHTQSDSPFLNPLKTVQVLMNTVTLIRAGGSIDPTGH 180				
DB	121	AFAGELAPOLITHTQSDSPFLNPLKTVQVLMNTVTLIRAGGSIDPTGH 180				
QY	181	QTAFRELEVFNPQSLCLGRKQDSCSLTALPSELYSADNVLGAVSLAMLT 240				
DB	181	QTAFRELEVFNPQSLCLGRKQDSCSLTALPSELYSADNVLGAVSLAMLT 240				
QY	241	RTFLQDQCPPEGRKRTDSHOWTLLSNAGQFTLQETFEVARSNPTLQDKTA 300				
DB	241	RTFLQDQCPPEGRKRTDSHOWTLLSNAGQFTLQETFEVARSNPTLQDKTA 300				

QY 301 LTPHPPOKQVGTLPSTVLTAGHETNLANIGSLSNWTLFQDPDPTPGHLYVERW 360
DB 301 LTPHPPOKQVGTLPSTVLTAGHETNLANIGSLSNWTLFQDPDPTPGHLYVERW 360
QY 361 RELEDSNOMIOVLVFTQLOQRDKTPSLNTPPGVYKLTLAGCERNAGKCSLAGPTQ 420
DB 361 RELEDSNOMIOVLVFTQLOQRDKTPSLNTPPGVYKLTLAGCERNAGKCSLAGPTQ 420
QY 421 IYNERTIPACSL 432
DB 421 IYNERTIPACSL 432

Search completed: December 18, 2003, 08:49:28
Job time : 1 secs